SEQUENCE LISTING

<110> CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE

<120> NOVEL ANTI-ANGIOGENIC AGENT AND ITS USE, IN PARTICULAR WITHIN THE FRAMEWORK OF THE TREATMENT OF CANCER

<130> WOB 03 AW CNR GIOG

<150> FR 03/09506
<151> 2004-08-01

<160> 12

<170> PatentIn version 3.1

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<213> homo sapiens

<220>
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<222> (73)..(1143)
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Met Gln Ser Val Gln Ser Thr Ser Phe Cys Leu Arg Lys
1 5 10

cag tgc ctt tgc ctg acc ttc ctg ctt ctc cat ctc ctg gga cag gtc 159
Gln Cys Leu Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val
15 20 25

gct gcg act cag cgc tgc cct ccc cag tgc ccg ggc cgg tgc cct gcg 207
Ala Ala Thr Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala
30 35 40 45

acg ccg ccg acc tgc gcc ccc ggg gtg cgc gcg gtg ctg gac ggc tgc 255
Thr Pro Pro Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys
50 55 60

tca tgc tgt ctg gtg tgt gcc cgc cag cgt ggc gag agc tgc tca gat 303
Ser Cys Cys Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp
65 70 75

ctg gag cca tgc gac gag agc agt ggc ctc tac tgt gat cgc agc gcg 351
Leu Glu Pro Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala
80 85 90

gac ccc agc aac cag act ggc atc tgc acg gcg gta gag gga gat aac 399
Asp Pro Ser Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn
95 100 105

tgt gtg ttc gat ggg gtc atc tac cgc agt gga gag aaa ttt cag cca 447
Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro
110 115 120 125

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agc tgc aaa ttc cag tgc acc tgc aga gat ggg cag att ggc tgt gtg      495
Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val
                130                 135                 140

ccc cgc tgt cag ctg gat gtg cta ctg cct gag cct aac tgc cca gct      543
Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala
            145                 150                 155

cca aga aaa gtt gag gtg cct gga gag tgc tgt gaa aag tgg atc tgt      591
Pro Arg Lys Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys
        160                 165                 170

ggc cca gat gag gag gat tca ctg gga ggc ctt acc ctt gca gct tac      639
Gly Pro Asp Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr
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agg cca gaa gcc acc cta gga gta gaa gtc tct gac tca agt gtc aac      687
Arg Pro Glu Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn
190                 195                 200                 205

tgc att gaa cag acc aca gag tgg aca gca tgc tcc aag agc tgt ggt      735
Cys Ile Glu Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly
                210                 215                 220

atg ggg ttc tcc acc cgg gtc acc aat agg aac cgt caa tgt gag atg      783
Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met
            225                 230                 235

ctg aaa cag act cgg ctc tgc atg gtg cgg ccc tgt gaa caa gag cca      831
Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro
        240                 245                 250

gag cag cca aca gat aag aaa gga aaa aag tgt ctc cgc acc aag aag      879
Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys
    255                 260                 265

tca ctc aaa gcc atc cac ctg cag ttc aag aac tgc acc agc ctg cac      927
Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His
270                 275                 280                 285

acc tac aag ccc agg ttc tgt ggg gtc tgc agt gat ggc cgc tgc tgc      975
Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys
                290                 295                 300

act ccc cac aat acc aaa acc atc cag gca gag ttt cag tgc tcc cca     1023
Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro
            305                 310                 315

ggg caa ata gtc aag aag cca gtg atg gtc att ggg acc tgc acc tgt     1071
Gly Gln Ile Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys
        320                 325                 330

cac acc aac tgt cct aag aac aat gag gcc ttc ctc cag gag ctg gag     1119
His Thr Asn Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu
    335                 340                 345

ctg aag act acc aga ggg aaa atg taacctatca ctcaagaagc acacctacag    1173
Leu Lys Thr Thr Arg Gly Lys Met
350                 355
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<210> 2
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<212> PRT
<213> homo sapiens

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Cys Leu Thr Phe Leu Leu Leu His Leu Leu Gly Gln Val Ala Ala Thr
            20                  25                  30

Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro
        35                  40                  45

Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys
    50                  55                  60

Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro
65                  70                  75                  80

Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser
                85                  90                  95

Asn Gln Thr Gly Ile Cys Thr Ala Val Glu Gly Asp Asn Cys Val Phe
            100                 105                 110

Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe Gln Pro Ser Cys Lys
        115                 120                 125

Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly Cys Val Pro Arg Cys
    130                 135                 140

Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys Pro Ala Pro Arg Lys
145                 150                 155                 160

Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp Ile Cys Gly Pro Asp
                165                 170                 175
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```
Glu Glu Asp Ser Leu Gly Gly Leu Thr Leu Ala Ala Tyr Arg Pro Glu
            180                 185                 190

Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser Val Asn Cys Ile Glu
        195                 200                 205

Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly Met Gly Phe
    210                 215                 220

Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met Leu Lys Gln
225                 230                 235                 240

Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln Glu Pro Glu Gln Pro
                245                 250                 255

Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr Lys Lys Ser Leu Lys
            260                 265                 270

Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser Leu His Thr Tyr Lys
        275                 280                 285

Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg Cys Cys Thr Pro His
    290                 295                 300

Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys Ser Pro Gly Gln Ile
305                 310                 315                 320

Val Lys Lys Pro Val Met Val Ile Gly Thr Cys Thr Cys His Thr Asn
                325                 330                 335

Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu Leu Glu Leu Lys Thr
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Thr Arg Gly Lys Met
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<222> (1)..(216)
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Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro
1               5                   10                  15

acc tgc gcc ccc ggg gtg cgc gcg gtg ctg gac ggc tgc tca tgc tgt       96
Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys
            20                  25                  30
```

```
ctg gtg tgt gcc cgc cag cgt ggc gag agc tgc tca gat ctg gag cca      144
Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro
        35                  40                  45

tgc gac gag agc agt ggc ctc tac tgt gat cgc agc gcg gac ccc agc      192
Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser
    50                  55                  60

aac cag act ggc atc tgc acg gcg                                      216
Asn Gln Thr Gly Ile Cys Thr Ala
65                  70
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<210> 4
<211> 72
<212> PRT
<213> artificial sequence

<220>
<223> fragment of NOV protein

<400> 4

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Gln Arg Cys Pro Pro Gln Cys Pro Gly Arg Cys Pro Ala Thr Pro Pro
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Thr Cys Ala Pro Gly Val Arg Ala Val Leu Asp Gly Cys Ser Cys Cys
            20                  25                  30

Leu Val Cys Ala Arg Gln Arg Gly Glu Ser Cys Ser Asp Leu Glu Pro
        35                  40                  45

Cys Asp Glu Ser Ser Gly Leu Tyr Cys Asp Arg Ser Ala Asp Pro Ser
    50                  55                  60

Asn Gln Thr Gly Ile Cys Thr Ala
65                  70
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<210> 5
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<212> DNA
<213> artificial sequence

<220>
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gat aac tgt gtg ttc gat ggg gtc atc tac cgc agt gga gag aaa ttt       48
Asp Asn Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe
1               5                   10                  15

cag cca agc tgc aaa ttc cag tgc acc tgc aga gat ggg cag att ggc       96
Gln Pro Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly
            20                  25                  30
```

```
tgt gtg ccc cgc tgt cag ctg gat gtg cta ctg cct gag cct aac tgc      144
Cys Val Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys
        35                  40                  45

cca gct cca aga aaa gtt gag gtg cct gga gag tgc tgt gaa aag tgg      192
Pro Ala Pro Arg Lys Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp
    50                  55                  60

atc tgt ggc                                                         201
Ile Cys Gly
65
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<210> 6
<211> 67
<212> PRT
<213> artificial sequence

<220>
<223> fragment of NOV protein

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Asp Asn Cys Val Phe Asp Gly Val Ile Tyr Arg Ser Gly Glu Lys Phe
1               5                   10                  15

Gln Pro Ser Cys Lys Phe Gln Cys Thr Cys Arg Asp Gly Gln Ile Gly
            20                  25                  30

Cys Val Pro Arg Cys Gln Leu Asp Val Leu Leu Pro Glu Pro Asn Cys
        35                  40                  45

Pro Ala Pro Arg Lys Val Glu Val Pro Gly Glu Cys Cys Glu Lys Trp
    50                  55                  60

Ile Cys Gly
65
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<210> 7
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<212> DNA
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Cys Ile Glu Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly
1               5                   10                  15

atg ggg ttc tcc acc cgg gtc acc aat agg aac cgt caa tgt gag atg       96
Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met
            20                  25                  30
```

```
ctg aaa cag act cgg ctc tgc atg gtg cgg ccc tgt gaa                    135
Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu
        35                  40                  45


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<212>  PRT
<213>  artificial sequence

<220>
<223>  fragment of NOV protein

<400>  8
Cys Ile Glu Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser Cys Gly
1               5                  10                  15

Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys Glu Met
            20                  25                  30

Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu
        35                  40                  45


<210>  9
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tgt ctc cgc acc aag aag tca ctc aaa gcc atc cac ctg cag ttc aag        48
Cys Leu Arg Thr Lys Lys Ser Leu Lys Ala Ile His Leu Gln Phe Lys
1               5                  10                  15

aac tgc acc agc ctg cac acc tac aag ccc agg ttc tgt ggg gtc tgc        96
Asn Cys Thr Ser Leu His Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys
            20                  25                  30

agt gat ggc cgc tgc tgc act ccc cac aat acc aaa acc atc cag gca       144
Ser Asp Gly Arg Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln Ala
        35                  40                  45

gag ttt cag tgc tcc cca ggg caa ata gtc aag aag cca gtg atg gtc       192
Glu Phe Gln Cys Ser Pro Gly Gln Ile Val Lys Lys Pro Val Met Val
    50                  55                  60

att ggg acc tgc acc tgt cac acc aac tgt cct                           225
Ile Gly Thr Cys Thr Cys His Thr Asn Cys Pro
65                  70                  75
```

<210> 10
<211> 75
<212> PRT
<213> artificial sequence

<220>
<223> fragment of NOV protein

<400> 10

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Asn Cys Thr Ser Leu His Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys
            20                  25                  30

Ser Asp Gly Arg Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln Ala
        35                  40                  45

Glu Phe Gln Cys Ser Pro Gly Gln Ile Val Lys Lys Pro Val Met Val
    50                  55                  60

Ile Gly Thr Cys Thr Cys His Thr Asn Cys Pro
65                  70                  75
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<213> Homo sapiens

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Ala Tyr Arg Pro Glu Ala Thr Leu Gly Val Glu Val Ser Asp Ser Ser
1               5                  10                  15

gtc aac tgc att gaa cag acc aca gag tgg aca gca tgc tcc aag agc       96
Val Asn Cys Ile Glu Gln Thr Thr Glu Trp Thr Ala Cys Ser Lys Ser
            20                  25                  30

tgt ggt atg ggg ttc tcc acc cgg gtc acc aat agg aac cgt caa tgt      144
Cys Gly Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys
        35                  40                  45

gag atg ctg aaa cag act cgg ctc tgc atg gtg cgg ccc tgt gaa caa      192
Glu Met Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln
    50                  55                  60

gag cca gag cag cca aca gat aag aaa gga aaa aag tgt ctc cgc acc      240
Glu Pro Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr
65                  70                  75                  80

aag aag tca ctc aaa gcc atc cac ctg cag ttc aag aac tgc acc agc      288
Lys Lys Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser
                85                  90                  95
```

```
ctg cac acc tac aag ccc agg ttc tgt ggg gtc tgc agt gat ggc cgc      336
Leu His Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg
            100                 105                 110

tgc tgc act ccc cac aat acc aaa acc atc cag gca gag ttt cag tgc      384
Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys
        115                 120                 125

tcc cca ggg caa ata gtc aag aag cca gtg atg gtc att ggg acc tgc      432
Ser Pro Gly Gln Ile Val Lys Lys Pro Val Met Val Ile Gly Thr Cys
    130                 135                 140

acc tgt cac acc aac tgt cct aag aac aat gag gcc ttc ctc cag gag      480
Thr Cys His Thr Asn Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu
145                 150                 155                 160

ctg gag ctg aag act acc aga ggg aaa atg                              510
Leu Glu Leu Lys Thr Thr Arg Gly Lys Met
                165                 170
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<210> 12
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<212> PRT
<213> Homo sapiens

<400> 12

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            20                  25                  30

Cys Gly Met Gly Phe Ser Thr Arg Val Thr Asn Arg Asn Arg Gln Cys
        35                  40                  45

Glu Met Leu Lys Gln Thr Arg Leu Cys Met Val Arg Pro Cys Glu Gln
    50                  55                  60

Glu Pro Glu Gln Pro Thr Asp Lys Lys Gly Lys Lys Cys Leu Arg Thr
65                  70                  75                  80

Lys Lys Ser Leu Lys Ala Ile His Leu Gln Phe Lys Asn Cys Thr Ser
                85                  90                  95

Leu His Thr Tyr Lys Pro Arg Phe Cys Gly Val Cys Ser Asp Gly Arg
            100                 105                 110

Cys Cys Thr Pro His Asn Thr Lys Thr Ile Gln Ala Glu Phe Gln Cys
        115                 120                 125

Ser Pro Gly Gln Ile Val Lys Lys Pro Val Met Val Ile Gly Thr Cys
    130                 135                 140

Thr Cys His Thr Asn Cys Pro Lys Asn Asn Glu Ala Phe Leu Gln Glu
145                 150                 155                 160

Leu Glu Leu Lys Thr Thr Arg Gly Lys Met
                165                 170
```